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CDN't.

Cytochrome c family heme-binding site signature
80-85 CAQCHA (SEQ ID NO: 744)--

In the claims:

~~Please replace the paragraph beginning at page 171, line 30, with the following rewritten paragraph:~~

--9. The composition of claim 7 comprising an analog peptide of eight, nine ten or eleven contiguous amino acids of Figure 2 (piece of SEQ ID NO:728).--

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~~Please replace the paragraph beginning at page 171, line 33, with the following rewritten paragraph:~~

--10. A composition of claim 7 comprising a CTL polypeptide epitope from Figure 2 (piece of SEQ ID NO:728).--

Please replace the paragraph beginning at page 172, line 1, with the following rewritten paragraph:

--12. A composition comprising a peptide region of at least 5 amino acids of Figure 2 (piece of SEQ ID NO:728) in any whole number increment up to 229 that includes an amino acid position selected from: an amino acid position having a value greater than 0.5 in the Hydrophilicity profile of Figure 5, an amino acid position having a value less than 0.5 in the Hydrophobicity profile of Figure 6; an amino acid position having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7; an amino acid position having a value greater than 0.5 in the Average Flexibility profile on Figure 8; or an amino acid position having a value greater than 0.5 in the Beta-turn profile of Figure 9.--

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Please replace the paragraph beginning at page 173, line 16, with the following rewritten paragraph:

A21 --29. A composition of claim 28 comprising a polynucleotide from position number 13 through number 702 of Figure 2 (piece of SEQ ID NO:727).--

Please replace the paragraph beginning at page 173, line 21, with the following rewritten paragraph:

A22 --31. A composition of claim 28 comprising a polynucleotide of Figure 2 (piece of SEQ ID NO:727) in a human unit dose form.--

Please replace the paragraph beginning at page 173, line 26, with the following rewritten paragraph:

--33. A composition claim 28 comprising a polynucleotide that encodes an 85P1B3-related protein that is at least 90% homologous to the entire amino acid sequence shown in Figure 2 (SEQ ID NO:727).--

A23 ~~Please replace the paragraph beginning at page 173, line 30, with the following rewritten paragraph.~~

--34. The composition of claim 33, wherein the polynucleotide encodes an 85P1B3-related protein that is at least 90% identical to the entire amino acid sequence shown in Figure 2 (SEQ ID NO:727).--

Please replace the paragraph beginning at page 173, line 36, with the following rewritten paragraph:

A24 --36. A composition of claim 28 comprising a polynucleotide that encodes a peptide region of at least 5 amino acids of Figure 2 (piece of SEQ ID NO:727) in any whole number increment up to 299 that includes an amino acid position selected from: an amino acid position

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cont.

having a value greater than 0.5 in the Hydrophilicity profile of Figure 5, an amino acid position having a value less than 0.5 in the Hydropathicity profile of Figure 6; an amino acid position having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7; an amino acid position having a value greater than 0.5 in the Average Flexibility profile on Figure 8; or an amino acid position having a value greater than 0.5 in the Beta-turn profile of Figure 9.--

Please replace the paragraph beginning at page 178, line 3, with the following rewritten paragraph:

--71. The assay of claim 68 for detecting the presence of an 85P1B3 polynucleotide in a biological sample comprising:

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contacting the sample with a polynucleotide probe that specifically hybridizes to a polynucleotide encoding an 85P1B3-related protein having the amino acid sequence of Figure 2 (SEQ ID NO:728); and,

detecting the presence of a hybridization complex formed by the hybridization of the probe with 85P1B3 polynucleotide in the sample, wherein the presence of the hybridization complex indicates the presence of 85P1B3 polynucleotide within the sample.--
